

SEQUENCE LISTING

<110> West, James W.
Brandt, Cameron S.
Jaspers, Stephen R.

<120> Production of Homotrimeric Fusion
Proteins

<130> 02-17

<140> 10/684,149

<141> 2003-10-10

<150> 60/417,801

<151> 2002-10-11

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> C-myc tag

<400> 1

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

1 5 10

<210> 2

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Hemagglutinin A epitope tag

<400> 2

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1 5

<210> 3
<211> 1377
<212> DNA
<213> Human

<220>
<221> CDS
<222> (14)...(892)

<400> 3
agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg 49
Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
1 5 10

agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg 97
Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
15 20 25

gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
30 35 40

ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc 193
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
45 50 55 60

acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc 241
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
65 70 75

aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc 289
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
80 85 90

tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc 337
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
95 100 105

agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga 385
Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
110 115 120

gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga tfg gag 433
Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu

125 130 135 140
 cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt 481
 His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser
 145 150 155
 gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt 529
 Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys
 160 165 170
 gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag 577
 Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys
 175 180 185
 agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt 625
 Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser
 190 195 200
 ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg 673
 Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val
 205 210 215 220
 agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag 721
 Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu
 225 230 235
 tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac 769
 Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp
 240 245 250
 ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg 817
 Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
 255 260 265
 cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg 865
 Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val
 270 275 280
 cct gcc cag gag ggg gcc cca ggt gca taaatggggg tcaggagggg 912
 Pro Ala Gln Glu Gly Gly Pro Gly Ala
 285 290
 aaaggaggag ggagagagat ggagaggagg ggagagagaa agagagggtgg ggagaggaga 972
 gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032
 gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga 1092
 gccagagaag gaaagagaca ggacagagaag gagagaggca gagagggaga gaggcagaga 1152

gggagagagg cagagagaca gagagggaga gaggacaga gagataga gcaggaggtc 1212
 ggggcactct gagtccagt tcccagtcca gctgtaggtc gtcacacct aaccacacgt 1272
 gcaataaagt cctcgtgctt gctgctcaca gcccccgaga gccctctc ctggagaata 1332
 aaacctttgg cagctgccct tctcaaaaa aaaaaaaaaa aaaaa 1377

<210> 4
 <211> 293
 <212> PRT
 <213> Human

<400> 4
 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
 20 25 30
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu

275 280 285
 Gly Gly Pro Gly Ala
 290

<210> 5
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 5
 gggcctccag gccaccagg t 21

<210> 6
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 6
 tcacattgga gccactagga a 21

<210> 7
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 7
 acaggtgtcc aggggaattca tataggccgg ccaccatgga tgcaatgaag agaggg 56

<210> 8
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 8

accctcaggc atcgaaacccg aacccgaacc ggatcc

36

<210> 9

<211> 118

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 9

gatcggatcc atgcccgaag ctgacccctaa aacagttcaa gaccttaccg gcgtatgcc 60
gagctcctcg caagagatcg aagataagtt tcagactatg agcgacacaa tcattgag 118

<210> 10

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 10

agaatgcatg acatgagctc caggatagat gaccttgaga aaaatatagc agatttaatg 60
acgcaagctg gtgtggaaga gttggaagga agtggttcta 100

<210> 11

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 11

gatctagaac caactcttc caactcttc acaccagctt gcgtcattaa atctgctata 60
ttttctcaa ggtcatctat cctggagctc atgtcatga ttctetcaat 110

<210> 12

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 12
gatttggctg ctcatagtct gaaacttacc ttgcattctt tgcaggagcg tctggactac 60
gctggtaagg tcttgaactg ttttaggac agtttcggcc atggatcc 108

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 13
cacacgtacg aagatggatg caatgaagag agg 33

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
ggttagatct cgaacccgaa cccgaaccgg 30

<210> 15
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
ctagaaataa tttgttttaa cttaagaag gagatatata tatggctatg agatcctgcc 60
cc 62

<210> 16
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 16
tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ctagtgtagg tgaaggatg 60
ggcc 64

<210> 17
<211> 516
<212> DNA
<213> Artificial Sequence

<220>
<223> TACI-HSBP fragment

<400> 17
atggctatga gatcctgccc cgaagagcag tactgggatc ctctgctggg tacctgcatg 60
tctgcacaaa ccatttgcaa ccatcagagc cagcgacct gtgcagcctt ctgcaggta 120
ctcagctgcc gcaaggagca aggcgaagtc tatgaccatc tctgagggga ctgcatcagc 180
tgtgcctcca tctgtggaca gcaccctaag caatgtgcat acttctgtga gaacaagctc 240
aggagcggat cgggttcggg ttccgggttcg agatccatgg ccgaaactga tcctaaaaca 300
gtcaagacc ttaccagcgt agtcagacg ctctgcaag agatgcaaga taagtttcag 360
actatgagcg accaaatcat tgagagaatc gatgacatga gctccaggat agatgacctt 420
gagaaaaata tagcagattt aatgacgcaa gctggtgtgg aagagttgga aggaagttgt 480
tctagatccg gtggccatca ccatccat cactga 516

<210> 18
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> TACI-HSBP fragment

<400> 18
Met Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
1 5 10 15
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80
Arg Ser Gly Ser Gly Ser Gly Ser Arg Ser Met Ala Glu Thr
85 90 95
Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val Gln Thr Leu Leu

100 105 110
 Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp Gln Ile Ile Glu
 115 120 125
 Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu Glu Lys Asn Ile
 130 135 140
 Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu Glu Gly Ser Gly
 145 150 155 160
 Ser Arg Ser Gly Gly His His His His His
 165 170

<210> 19
 <211> 480
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NC-1 fragment

<220>
 <221> CDS
 <222> (1)...(480)

<400> 19
 atg cct gag ggt ttt ata aag gca ggc caa agg ccc agt ctt tct ggg 48
 Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
 1 5 10 15

 acc cct ctt gtt agt gcc aac cag cgg gta aca gga atg cct gtg tct 96
 Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
 20 25 30

 gct ttt act gtt att ctc tcc aaa gct tac cca gca ata gga act ccc 144
 Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
 35 40 45

 ata cca ttt gat aaa att ttg tat aac agg caa cag cat tat gac cca 192
 Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln His Tyr Asp Pro
 50 55 60

 agg act gga atc ttt act tgt cag ata cca gga ata tac tat ttt tca 240
 Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
 65 70 75 80

 tac cac gtg cat gtg aaa ggg act cat gtt tgg gta ggc ctg tat aag 288
 Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys

85

90

95

aat ggc acc cct gta atg tac acc tat gat gaa tac acc aaa ggc tac 336
 Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
 100 105 110

ctg gat cag gct tca ggg agt gcc atc atc gat ctc aca gaa aat gac 384
 Leu Asp Gln Ala Ser Gly Ser Ala Ile Asp Leu Thr Glu Asn Asp
 115 120 125

cag gtg tgg ctc cag ctt ccc aat gcc gag tca aat ggc cta tac tcc 432
 Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
 130 135 140

tct gag tat gtc cac tcc tct ttc tca gga ttc cta gtg gct cca atg 480
 Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
 145 150 155 160

<210> 20

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> NC-1 fragment

<400> 20

Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
 1 5 10 15
 Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
 20 25 30
 Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
 35 40 45
 Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
 50 55 60
 Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
 65 70 75 80
 Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
 85 90 95
 Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
 100 105 110
 Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
 115 120 125
 Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser

<400> 22

Met Ala Glu Thr Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val

1 5 10 15

Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp

20 25 30

Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu

35 40 45

Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu

50 55 60

Glu

65

<210> 23

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> RYIRS tag

<400> 23

Arg Tyr Ile Arg Ser

1 5